

SEQUENCE LISTING

<110> Kato, Seishi
Sekine, Shingo

<120> HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND
CDNAS ENCODING THESE PROTEINS

<130> GIN-6710CPUS

<140> 09/529,100

<141> 2000-08-21

<150> JP 0276269

<151> 1997-10-08

<150> PCT/JP98/04474

<151> 1998-10-05

<160> 28

<170> PatentIn Ver. 2.0

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<212> PRT

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Ile Pro Ala Ser Phe Thr Ser Ala Lys Ser Val Phe Ser Ser Lys Ala
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Arg Ile Asn Asn Lys Tyr Asp Glu Thr Tyr Pro Pro Leu Pro Val Glu
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Glu Ile Ile Lys Arg Ser Glu Phe Val Ile Gly Gln Glu Val Ala Tyr
100 105 110

Asn Leu Leu Val Asn Asn Cys Glu His Phe Val Thr Leu Leu Arg Tyr
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Gly Glu Gly Val Ser Glu Gln Ala Asn Arg Ala Ile Ser Thr Val Glu
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 35 40 45

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 Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala
 85 90 95

 Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn
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 Cys Glu His Phe Val Thr Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys
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 Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
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 Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val
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 85 90 95
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Gly	Cys	Gly	Ser	Gly	Leu	Pro	Gly	Lys	Asn	Asp	Arg	Gly	Leu	Asp	Leu
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His	Gly	Leu	Leu	Ala	Phe	Ile	Gln	Leu	Gln	Gln	Cys	Ala	Gln	Asp	Arg
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275 280 285

Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly Gly Ala Ala Gly His Gln
290 295 300

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Glu Glu Lys Ala Ser Val Gly Pro Trp Leu Leu Ala Leu Phe Ile Phe
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Gly Met
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atcaacatag cacctgtaga tggcattcct gcgtccttta caagcgccaa gtctgtattc 180
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gagtaccccg gggctggctc ctccagtgtc ttctcagtcc tgagcaacag tgcagaggtg 180

aaacgggagc gcctggaaga tgtggtggga ggctgttgct atcgggtcaa caacagcttg 240

gaccatgagt accaaccacg gcccggtggag gtgatcatca gttctgcgaa ggagatgggt 300

ggtcagaaga tgaagtacag tattgtgagc aggaactgtg agcactttgt caccagctg 360

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acggcgcttg gaatcctggt tgttgctgga tgctcttttg cgattaggag ataccaaaaa 480

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gtg 423

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gatgacggat gctccccgaa caagatgaag acagtgaagt gcgcgccggg cgtggacgtc 180
tgcaccgagg ccgtggggggc ggtggagacc atccacggac aattctcgct ggcagtgcgg 240
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tgcgagaaga agaccccggc ttgagagtga g atg gcg ttt aat gat tgc ttc 232
Met Ala Phe Asn Asp Cys Phe
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agt ttg aac tac cct ggc aac ccc tgc cca ggg gac ttg atc gaa gtg 280
Ser Leu Asn Tyr Pro Gly Asn Pro Cys Pro Gly Asp Leu Ile Glu Val
10 15 20
ttc cgt cct ggc tat cag cac tgg gcc ctg tac ttg ggt gat ggt tac 328
Phe Arg Pro Gly Tyr Gln His Trp Ala Leu Tyr Leu Gly Asp Gly Tyr
25 30 35
gtt atc aac ata gca cct gta gat ggc att cct gcg tcc ttt aca agc 376
Val Ile Asn Ile Ala Pro Val Asp Gly Ile Pro Ala Ser Phe Thr Ser
40 45 50 55
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Ala Lys Ser Val Phe Ser Ser Lys Ala Leu Val Lys Met Gln Leu Leu
60 65 70

aag gat gtt gtg gga aat gac aca tac aga ata aac aat aaa tac gat 472
 Lys Asp Val Val Gly Asn Asp Thr Tyr Arg Ile Asn Asn Lys Tyr Asp
 75 80 85

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 Glu Thr Tyr Pro Pro Leu Pro Val Glu Glu Ile Ile Lys Arg Ser Glu
 90 95 100

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 Phe Val Ile Gly Gln Glu Val Ala Tyr Asn Leu Leu Val Asn Asn Cys
 105 110 115

gaa cat ttt gtg aca ttg ctt cgc tat gga gaa gga gtt tca gag cag 616
 Glu His Phe Val Thr Leu Leu Arg Tyr Gly Glu Gly Val Ser Glu Gln
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 Val Phe Ser Phe Leu Gly Leu Phe Pro Lys Gly Gln Arg Ala Lys Tyr
 155 160 165

tat taacaattta ccaaagagat attgatattg aaggaatttg ggaggaggaa 765
 Tyr

aagaaacctg ggggtgaatac ttatttttcag tgcattcatta ctgttccaga ttcctatgat 825

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 35 40 45

Ile Pro Ala Ser Phe Thr Ser Ala Lys Ser Val Phe Ser Ser Lys Ala
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Arg Ile Asn Asn Lys Tyr Asp Glu Thr Tyr Pro Pro Leu Pro Val Glu
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Glu Ile Ile Lys Arg Ser Glu Phe Val Ile Gly Gln Glu Val Ala Tyr

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130	135	140
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Lys Gly Gln Arg Ala Lys Tyr Tyr		
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Pro Gly Asp Leu Ile Glu Ile Phe Arg Leu Gly Tyr Glu His Trp Ala
10 15 20 25

ctg tat ata gga gat ggc tac gtg atc cat ctg gct cct cca agt gag 147
Leu Tyr Ile Gly Asp Gly Tyr Val Ile His Leu Ala Pro Pro Ser Glu
30 35 40

tac ccc ggg gct ggc tcc tcc agt gtc ttc tca gtc ctg agc aac agt 195
Tyr Pro Gly Ala Gly Ser Ser Ser Val Phe Ser Val Leu Ser Asn Ser
45 50 55

gca gag gtg aaa cgg gag cgc ctg gaa gat gtg gtg gga ggc tgt tgc 243
Ala Glu Val Lys Arg Glu Arg Leu Glu Asp Val Val Gly Gly Cys Cys
60 65 70

tat cgg gtc aac aac agc ttg gac cat gag tac caa cca cgg ccc gtg 291
Tyr Arg Val Asn Asn Ser Leu Asp His Glu Tyr Gln Pro Arg Pro Val
75 80 85

gag gtg atc atc agt tct gcg aag gag atg gtt ggt cag aag atg aag 339
Glu Val Ile Ile Ser Ser Ala Lys Glu Met Val Gly Gln Lys Met Lys
90 95 100 105

tac agt att gtg agc agg aac tgt gag cac ttt gtc acc cag ctg aga 387
Tyr Ser Ile Val Ser Arg Asn Cys Glu His Phe Val Thr Gln Leu Arg
110 115 120

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 Tyr Gly Lys Ser Arg Cys Lys Gln Val Glu Lys Ala Lys Val Glu Val
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 Gly Val Ala Thr Ala Leu Gly Ile Leu Val Val Ala Gly Cys Ser Phe
 140 145 150

gcg att agg aga tac caa aaa aaa gcg aca gcc tgaagcagcc acaaaatcct 536
 Ala Ile Arg Arg Tyr Gln Lys Lys Ala Thr Ala
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 Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Glu Arg
 50 55 60
 Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu
 65 70 75 80
 Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala
 85 90 95
 Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn
 100 105 110
 Cys Glu His Phe Val Thr Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys
 115 120 125
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Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile
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Pro Asp Gly Thr Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile
15 20 25

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Ala Ser Val Ala Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn
30 35 40

cct ccg ggc acc ttc ctt gaa gga gtg gct aag gtt gga caa tac acg 253
Pro Pro Gly Thr Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr
45 50 55 60

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Phe Thr Ala Ala Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile
65 70 75

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Ser Ala His Val Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu
80 85 90

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95 100 105

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110 115 120

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Val Lys Met Gly Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys
125 130 135 140

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 50 55 60
 Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val
 65 70 75 80
 Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala
 85 90 95
 Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr Gly Ile Gly Ala
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 Pro Asp Glu Leu Leu Pro Lys Gly Asp Ala Glu Lys Pro Glu Glu Glu
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 Leu Glu Glu Asp Asp Asp Glu Glu Leu Asp Glu Thr Leu Ser Glu Arg
 35 40 45

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 Leu Trp Gly Leu Thr Glu Met Phe Pro Glu Arg Val Arg Ser Ala Ala
 50 55 60

gga gcc act ttt gat ctt tcc ctc ttt gtg gct cag aaa atg tac agg 241
 Gly Ala Thr Phe Asp Leu Ser Leu Phe Val Ala Gln Lys Met Tyr Arg
 65 70 75

ttt tcc agg gca gcc ttg tgg att ggg acc act tcc ttt atg atc ctg 289
 Phe Ser Arg Ala Ala Leu Trp Ile Gly Thr Thr Ser Phe Met Ile Leu
 80 85 90 95

gtt ctt ccc gtt gtc ttt gag acg gag aag ttg caa atg gag caa cag 337
 Val Leu Pro Val Val Phe Glu Thr Glu Lys Leu Gln Met Glu Gln Gln
 100 105 110

cag caa ctg cag cag cgg cag ata ctt cta gga cct aac aca ggg ctc 385
 Gln Gln Leu Gln Gln Arg Gln Ile Leu Leu Gly Pro Asn Thr Gly Leu
 115 120 125

tca gga gga atg cca ggg gct cta ccc tca ctt cct gga aag atc 430
 Ser Gly Gly Met Pro Gly Ala Leu Pro Ser Leu Pro Gly Lys Ile
 130 135 140

tagattgtta ttgctgtttg agctgtctca gtgggataag tttgaaattc aagtgtttga 490
 actgctgata atttggattt tttttttttt ttttaacttt ggcacattga tctatctaaa 550
 cccggtgggg agaattatcc ccacattgtc tcatggaaag actcaacttg caactgtgcc 610
 ctccacacta tccttacttc tgtctccact ctgataccag agtgcagcca tgcagacggt 670
 tattccagct ctggtcaccg gactcctttc accaaattgc tcctaactgg aagatctcac 730
 tttccccttg tggggtagga accgatgcca gtgggaggga tgtgcccctg accattaacg 790
 actgtttttt tttttttttt ttaaagaatg gagttgttgg ggcgggacat gcacacaatg 850
 tgaaacagac aaaatgcatt acacctgtag tgtaaagtgg ccactatgaa tccctatgta 910
 tgagaggagg gaggcaggct gcagcttcag ccacagaatg gggactatgg aagacagcag 970
 gagctcattt cctctgcaca ttccggctgt tagacctgtg tgtgtgttta aaaaaagaga 1030
 agtcagtgtc cactttttgt atttaaatat taataatgat tccaactg 1078

<210> 20

<211> 142

<212> PRT

<213> Homo sapiens

<400> 20

Met Ala Ala Ala Val Ala Ala Ala Gly Ala Gly Glu Pro Gln Ser Pro
 1 5 10 15

Asp Glu Leu Leu Pro Lys Gly Asp Ala Glu Lys Pro Glu Glu Glu Leu

			20				25				30						
Glu	Glu	Asp	Asp	Asp	Glu	Glu	Leu	Asp	Glu	Thr	Leu	Ser	Glu	Arg	Leu		
		35					40					45					
Trp	Gly	Leu	Thr	Glu	Met	Phe	Pro	Glu	Arg	Val	Arg	Ser	Ala	Ala	Gly		
50						55					60						
Ala	Thr	Phe	Asp	Leu	Ser	Leu	Phe	Val	Ala	Gln	Lys	Met	Tyr	Arg	Phe		
65					70					75					80		
Ser	Arg	Ala	Ala	Leu	Trp	Ile	Gly	Thr	Thr	Ser	Phe	Met	Ile	Leu	Val		
				85					90					95			
Leu	Pro	Val	Val	Phe	Glu	Thr	Glu	Lys	Leu	Gln	Met	Glu	Gln	Gln	Gln		
		100						105					110				
Gln	Leu	Gln	Gln	Arg	Gln	Ile	Leu	Leu	Gly	Pro	Asn	Thr	Gly	Leu	Ser		
		115				120						125					
Gly	Gly	Met	Pro	Gly	Ala	Leu	Pro	Ser	Leu	Pro	Gly	Lys	Ile				
130						135					140						

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<210> 21
<211> 1310
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (82)..(1119)
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<400> 21
actcatcctg ggctcaggta agagggcccg agctcggagg cggcacatcc aggggggacg 60
ccaagggagc aggacggagc c atg gac ccc gcc agg aaa gca ggt gcc cag 111
                        Met Asp Pro Ala Arg Lys Ala Gly Ala Gln
                        1                               5                               10
gcc atg atc tgg act gca ggc tgg ctg ctg ctg ctg ctg ctt cgc gga 159
Ala Met Ile Trp Thr Ala Gly Trp Leu Leu Leu Leu Leu Leu Arg Gly
                        15                               20                               25
gga gcg cag gcc ctg gag tgc tac agc tgc gtg cag aaa gca gat gac 207
Gly Ala Gln Ala Leu Glu Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp
                        30                               35                               40
gga tgc tcc ccg aac aag atg aag aca gtg aag tgc gcg ccg ggc gtg 255
Gly Cys Ser Pro Asn Lys Met Lys Thr Val Lys Cys Ala Pro Gly Val
                        45                               50                               55
gac gtc tgc acc gag gcc gtg ggg gcg gtg gag acc atc cac gga caa 303
Asp Val Cys Thr Glu Ala Val Gly Ala Val Glu Thr Ile His Gly Gln
                        60                               65                               70
ttc tcg ctg gca gtg cgg ggt tgc ggt tcg gga ctc ccc ggc aag aat 351

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Phe 75	Ser	Leu	Ala	Val	Arg 80	Gly	Cys	Gly	Ser	Gly 85	Leu	Pro	Gly	Lys	Asn 90	
gac Asp	cgc Arg	ggc Gly	ctg Leu	gat Asp 95	ctt Leu	cac His	ggg Gly	ctt Leu 100	ctg Leu	gcg Ala	ttc Phe	atc Ile	cag Gln	ctg Leu 105	cag Gln	399
caa Gln	tgc Cys	gct Ala	cag Gln 110	gat Asp	cgc Arg	tgc Cys	aac Asn 115	gcc Ala	aag Lys	ctc Leu	aac Asn	ctc Leu	acc Thr 120	tcg Ser	cgg Arg	447
gcg Ala	ctc Leu	gac Asp 125	ccg Pro	gca Ala	ggt Gly	aat Asn 130	gag Glu	agt Ser 135	gca Ala	tac Tyr	ccg Pro	ccc Pro	aac Asn	ggc Gly	gtg Val	495
gag Glu 140	tgc Cys	tac Tyr	agc Ser	tgt Cys	gtg Val	ggc Gly 145	ctg Leu	agc Ser	cgg Arg	gag Glu 150	gcg Ala	tgc Cys	cag Gln	ggc Gly	aca Thr	543
tcg Ser 155	ccg Pro	ccg Pro	gtc Val	gtg Val	agc Ser 160	tgc Cys	tac Tyr	aac Asn	gcc Ala 165	agc Ser	gat Asp	cat His	gtc Val	tac Tyr	aag Lys 170	591
ggc Gly	tgc Cys	ttc Phe	gac Asp 175	ggc Gly	aac Asn	gtc Val	acc Thr	ttg Leu	acg Thr 180	gca Ala	gct Ala	aac Asn	gtg Val 185	act Thr	gtg Val	639
tcc Ser	ttg Leu	cct Pro	gtc Val 190	cgg Arg	ggc Gly	tgt Cys	gtc Val	cag Gln 195	gat Asp	gaa Glu	ttc Phe	tgc Cys	act Thr 200	cgg Arg	gat Asp	687
gga Gly	gta Val	aca Thr 205	ggc Gly	cca Pro	ggg Gly	ttc Phe 210	acg Thr	ctc Leu	agt Ser	ggc Gly	tcc Ser	tgt Cys 215	tgc Cys	cag Gln	ggg Gly	735
tcc Ser 220	cgc Arg	tgt Cys	aac Asn	tct Ser	gac Asp	ctc Leu 225	cgc Arg	aac Asn	aag Lys	acc Thr 230	tac Tyr	ttc Phe	tcc Ser	cct Pro	cga Arg	783
atc Ile 235	cca Pro	ccc Pro	ctt Leu	gtc Val	cgg Arg 240	ctg Leu	ccc Pro	cct Pro	cca Pro	gag Glu 245	ccc Pro	acg Thr	act Thr	gtg Val	gcc Ala 250	831
tca Ser	acc Thr	aca Thr	tct Ser	gtc Val 255	acc Thr	act Thr	tct Ser	acc Thr	tcg Ser 260	gcc Ala	cca Pro	gtg Val	aga Arg	ccc Pro 265	aca Thr	879
tcc Ser	acc Thr	acc Thr	aaa Lys 270	ccc Pro	atg Met	cca Pro	gcg Ala 275	cca Pro	acc Thr	agt Ser	cag Gln	act Thr	ccg Pro 280	aga Arg	cag Gln	927
gga Gly	gta Val	gaa Glu 285	cac His	gag Glu	gcc Ala	tcc Ser 290	cgg Arg	gat Asp	gag Glu	gag Glu	ccc Pro	agg Arg 295	ttg Leu	act Thr	gga Gly	975
ggc Gly	gcc Ala	gct Ala	ggc Gly	cac His	cag Gln	gac Asp	cgc Arg	agc Ser	aat Asn	tca Ser	ggg Gly	cag Gln	tat Tyr	cct Pro	gca Ala	1023

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      300              305              310
aaa ggg ggg ccc cag cag ccc cat aat aaa ggc tgt gtg gct ccc aca 1071
Lys Gly Gly Pro Gln Gln Pro His Asn Lys Gly Cys Val Ala Pro Thr
315              320              325              330

gct gga ttg gca gcc ctt ctg ttg gcc gtg gct gct ggt gtc cta ctg 1119
Ala Gly Leu Ala Ala Leu Leu Leu Ala Val Ala Ala Gly Val Leu Leu
335              340              345

tgagcttctc cacctggaaa tttccctctc acctacttct ctggccctgg gtacccctct 1179
tctcatcact tcctgttccc accactggac tgggctggcc cagcccctgt tttccaaca 1239
ttccccagta tccccagctt ctgctgcgct ggtttgcggc tttgggaaat aaaataaccgt 1299
tgtatatatt c 1310

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<210> 22
 <211> 346
 <212> PRT
 <213> Homo sapiens

<400> 22

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Met Asp Pro Ala Arg Lys Ala Gly Ala Gln Ala Met Ile Trp Thr Ala
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Gly Trp Leu Leu Leu Leu Leu Leu Arg Gly Gly Ala Gln Ala Leu Glu
20              25              30

Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser Pro Asn Lys
35              40              45

Met Lys Thr Val Lys Cys Ala Pro Gly Val Asp Val Cys Thr Glu Ala
50              55              60

Val Gly Ala Val Glu Thr Ile His Gly Gln Phe Ser Leu Ala Val Arg
65              70              75              80

Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn Asp Arg Gly Leu Asp Leu
85              90              95

His Gly Leu Leu Ala Phe Ile Gln Leu Gln Gln Cys Ala Gln Asp Arg
100             105             110

Cys Asn Ala Lys Leu Asn Leu Thr Ser Arg Ala Leu Asp Pro Ala Gly
115             120             125

Asn Glu Ser Ala Tyr Pro Pro Asn Gly Val Glu Cys Tyr Ser Cys Val
130             135             140

Gly Leu Ser Arg Glu Ala Cys Gln Gly Thr Ser Pro Pro Val Val Ser
145             150             155             160

Cys Tyr Asn Ala Ser Asp His Val Tyr Lys Gly Cys Phe Asp Gly Asn
165             170             175

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Val Thr Leu Thr Ala Ala Asn Val Thr Val Ser Leu Pro Val Arg Gly
 180 185 190
 Cys Val Gln Asp Glu Phe Cys Thr Arg Asp Gly Val Thr Gly Pro Gly
 195 200 205
 Phe Thr Leu Ser Gly Ser Cys Cys Gln Gly Ser Arg Cys Asn Ser Asp
 210 215 220
 Leu Arg Asn Lys Thr Tyr Phe Ser Pro Arg Ile Pro Pro Leu Val Arg
 225 230 235 240
 Leu Pro Pro Pro Glu Pro Thr Thr Val Ala Ser Thr Thr Ser Val Thr
 245 250 255
 Thr Ser Thr Ser Ala Pro Val Arg Pro Thr Ser Thr Thr Lys Pro Met
 260 265 270
 Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln Gly Val Glu His Glu Ala
 275 280 285
 Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly Gly Ala Ala Gly His Gln
 290 295 300
 Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys Gly Gly Pro Gln Gln
 305 310 315 320
 Pro His Asn Lys Gly Cys Val Ala Pro Thr Ala Gly Leu Ala Ala Leu
 325 330 335
 Leu Leu Ala Val Ala Ala Gly Val Leu Leu
 340 345

<210> 23
 <211> 781
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (342)..(539)

<400> 23
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 aaagcggcgg cgacggcggc gcgagaacga cccggcggcc agttctcttc ctctgcgca 120
 cctgccctgc tcggtcagtc agtcggcggc cggcgcccgg cttgtgctca gacctcgcg 180
 ttgcggcgcc caggcccagc ggccgtagct agcgtctggc ctgagaacct cggcgctccg 240
 gcggcgcggg caccacgagc ggagcctcgc agcggctcca gaggaggcag gcgagtgagc 300
 gagtccgagg ggtggccggg gcaggtggtg gcgccgcgaa g atg gtc gcc aag caa 356
 Met Val Ala Lys Gln

1

5

agg atc cgt atg gcc aac gag aag cac agc aag aac atc acc cag cgc 404
 Arg Ile Arg Met Ala Asn Glu Lys His Ser Lys Asn Ile Thr Gln Arg
 10 15 20

ggc aac gtc gcc aag acc tcg aga aat gcc ccc gaa gag aag gcg tct 452
 Gly Asn Val Ala Lys Thr Ser Arg Asn Ala Pro Glu Glu Lys Ala Ser
 25 30 35

gta gga ccc tgg tta ttg gct ctc ttc att ttt gtt gtc tgt ggt tct 500
 Val Gly Pro Trp Leu Leu Ala Leu Phe Ile Phe Val Val Cys Gly Ser
 40 45 50

gca att ttc cag att att caa agt atc agg atg ggc atg tgaagtgact 549
 Ala Ile Phe Gln Ile Ile Gln Ser Ile Arg Met Gly Met
 55 60 65

gaccttaaga tgtttccatt ctctgtgaa ttttaacttg aactcattcc tgatgtttga 609

taccctgggtt gaaaacaatt cagtaaagca tcctgcctca gaatgacttt cctatcatgc 669

ttcatgtgtc attccaaggt ttcttcatga gtcattccaa gttttctagt ccataccaca 729

gtgccttgca aaaaacacca catgaataaa gcaataaaat ttgattgtta ag 781

<210> 24

<211> 66

<212> PRT

<213> Homo sapiens

<400> 24

Met Val Ala Lys Gln Arg Ile Arg Met Ala Asn Glu Lys His Ser Lys
 1 5 10 15

Asn Ile Thr Gln Arg Gly Asn Val Ala Lys Thr Ser Arg Asn Ala Pro
 20 25 30

Glu Glu Lys Ala Ser Val Gly Pro Trp Leu Leu Ala Leu Phe Ile Phe
 35 40 45

Val Val Cys Gly Ser Ala Ile Phe Gln Ile Ile Gln Ser Ile Arg Met
 50 55 60

Gly Met
 65

<210> 25

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chimeric
 DNA-RNA oligonucleotide

<400> 25
ggggaattcg agga

14

<210> 26
<211> 162
<212> PRT
<213> Homo sapiens

<400> 26
Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
1 5 10 15
Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr
20 25 30
Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala
35 40 45
Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu
50 55 60
Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His
65 70 75 80
Asp Asp Lys Tyr Ser Pro Leu Pro Cys Thr Lys Ile Ile Gln Arg Ala
85 90 95
Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn
100 105 110
Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp
115 120 125
Gln Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu
130 135 140
Ala Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln
145 150 155 160
Lys Gln

<210> 27
<211> 162
<212> PRT
<213> Homo sapiens

<400> 27
Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
1 5 10 15
Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr
20 25 30

Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala
 35 40 45
 Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu
 50 55 60
 Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His
 65 70 75 80
 Asp Asp Lys Tyr Ser Pro Leu Pro Cys Thr Lys Ile Ile Gln Arg Ala
 85 90 95
 Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn
 100 105 110
 Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp
 115 120 125
 Gln Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu
 130 135 140
 Ala Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln
 145 150 155 160

Lys Gln

<210> 28
 <211> 64
 <212> PRT
 <213> Nematode

<400> 28
 Met Ala Pro Lys Gln Arg Met Thr Leu Ala Asn Lys Gln Phe Ser Lys
 1 5 10 15
 Asn Val Asn Asn Arg Gly Asn Val Ala Lys Ser Leu Lys Pro Ala Glu
 20 25 30
 Asp Lys Tyr Pro Ala Ala Pro Trp Leu Ile Gly Leu Phe Val Phe Val
 35 40 45
 Val Cys Gly Ser Ala Val Phe Glu Ile Ile Arg Tyr Val Lys Met Gly
 50 55 60